Docket JP920030152US1

Appl. No.: 10/699,024
Filing Date: October 31, 2003

REMARKS

This amendment, filed with a Request for Continued Examination, is in response to the final office action of 07/09/2008.

Objections

The Examiner objected to the specification because of a hyperlink embedded in the text. This has been corrected by amending the text so that it does not form an executable hyperlink.

35 USC 101

The Examiner rejected claims 2-11 under 35 USC 101 as being drawn to non-statutory subject matter. Specifically, the Examiner states:

> "However, dependent claims 2-11 are drawn to "the method of claim 1 further comprising" additional method steps for associating data, storing data, segmenting data, and identifying data. Because claims 2-11 do not set forth any limitations that require that they are performed before the final step recited in claim 1, the method steps of claim 2-11 could occur after the step for "presenting" data to a user in claim 1." Office action, 07/09/2008, page 3.

Applicants respectfully disagree that the step of providing the sequence to the user must be the last step in the method in order for the claim to recite statutory subject matter. Nor do Applicants admit that the steps must be performed in the order recited. Thus, Applicants traverse this rejection. Nevertheless, to advance this case to issue, the claims are amended, without prejudice, to make the steps of the dependent claims to be prior to the step of providing the reconstructed sequence to the user. This overcomes the Examiner's rejection under 35 USC 101.

35 USC 103(a)

The Examiner rejected claims 1-11 under 35 U.S.C. 103(a) as being unpatentable over Taylor et al. (Computer and Chemistry, 1999, Vol. 23, p.365-385), in view of Kalantery (US 5,832,272; Issued: Nov. 3, 1998), and in view of Huysmans et al. (Proteins: Structure, Function, and Genetics, 1991, Vol. 11, p. 59-76).

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Claim 1 is cancelled and new claim 14 is added to more clearly recite what is claimed as the invention. Support for claim 14 is found in the specification at least at paragraphs [0038] through [0043] and [0048] through [0054].
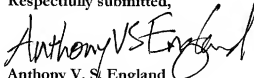
Taylor discloses specifying all the amino acids that can be matched to a pattern using UNIX software utilities. The matches to a pattern are found using a search routine. A match-set contains the amino acids that are matched. Information about the gaps between the amino acids is discarded. (Taylor, p.367, col. 2, par. 2-p. 368, col. 1, par. 2). Kalentery discloses parallel processing of a set of sequential instructions. The parallel processing is done in such a way that memory accesses occur in order. (Kalentery, Abstract, col. 2, ll. 16-31). Huysmans discloses a database for storing information about molecular structures of proteins. (Huysmans, Abstract, p. 62, col. 2, par. 2). Neither Taylor, Kalentery or Huysmans, either alone or in combination, teach or suggest the present invention as now recited.

Specifically, the references relied upon by the Examiner do not teach or suggest that a match-set data structure comprising a sequence identification and offset information is generated and stored for each matching subsequence, (specification, [0048]), wherein data redundancy corresponding to a subsequence being matched by more than one replet is avoided (specification, [0055]). (See claim 14: "a match-set data structure comprising a sequence identification to identify a sequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, and wherein redundant match-set data structures corresponding to subsequences being matched by more than one replet are not generated") Nor do the references teach or suggest "storing one or more variations for each of one or more matching subsequences, wherein a variation comprises a character in a subsequence that corresponds to a "don't care" character in a replet that matches the subsequence" (claim 14, specification, [0041]-[0042]). Nor do the references teach or suggest "concatenating, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence" (claim 14, specification, [0053]). Note that by teaching the discarding of the gap information, Taylor actually teaches away from the invention. Nor do the references teach or suggest "reconstructing a sequence from the stored match-set data, the stored variations, and the stored backbone sequence" (claim 14, specification, [0058]).

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REQUESTED ACTION

For these reasons, Applicant requests that all the claims be promptly allowed and that the application be passed to issuance.

Respectfully submitted,

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